

SEQUENCE LISTING

TECH CENTER 1600/2900

<110> EPIC BETARDE MACEUTICAL, INC.
 HIATT, ANDREW C.
 HEIN, MICH B.
 FITCHEN, JOHN H.



<120>	NOVEL	EPITHELIAL	TISSUE	IMAGING	AGENT
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<150> 09/005,167

<151> 1998-01-09

<150> 08/782,480

<151> 1997-01-10

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Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu 35 40 45

Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Pro Val Tyr His 50 55 60

Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp 65 70 75 80

Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser 85 90 95

Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala 100 105 110

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Leu Thr Pro Asp Ala Cys Tyr Pro Asp 130 135

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Ile Val Glu Arg Asn Val Arg Ile Ile Val Pro Leu Asn Ser Arg Glu 35 40 45

Asn Ile Ser Asp Pro Thr Ser Pro Met Arg Thr Lys Pro Val Tyr His 50 55 60

Leu Ser Asp Leu Cys Lys Lys Cys Asp Thr Thr Glu Val Glu Leu Glu 65 70 75 80

Asp Gln Val Val Thr Ala Ser Gln Ser Asn Ile Cys Asp Ser Asp Ala 85 90 95

Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Asn Arg Val

Lys Leu Ser Tyr Arg Gly Gln Thr Lys Met Val Glu Thr Ala Leu Thr 115 120 125

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Val Glu Arg Asn Ile Arg Ile Val Val Pro Leu Asn Asn Arg Glu Asn 35 40 45

Ile Ser Asp Pro Thr Ser Pro Leu Arg Arg Asn Pro Val Tyr His Leu 50 55 60

Ser Asp Val Cys Lys Lys Cys Asp Pro Val Glu Val Glu Leu Glu Asp 65 70 75 80

Gln Val Val Thr Ala Thr Gln Ser Asn Ile Cys Asn Glu Asp Asp Gly 85 90 95

Val Pro Glu Thr Cys Tyr Met Tyr Asp Arg Asn Lys Cys Tyr Thr Thr 100 105 110

Met Val Pro Leu Arg Tyr His Gly Glu Thr Lys Met Val Gln Ala Ala
115 120 125

Leu Thr Pro Asp Ser Cys Tyr Pro Asp 130 135 <210> 4

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Ala Asn Leu Cys Lys Lys Cys Asp Pro Thr Glu Ile Glu Leu Asp Asn 65 70 75 80

Gln Val Phe Thr Ala Ser Gln Ser Asn Ile Cys Pro Asp Asp Asp Tyr 85 90 95

Ser Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Thr Leu 100 105 110

Val Pro Ile Thr His Arg Gly Val Thr Arg Met Val Lys Ala Thr Leu 115 120 125

Thr Pro Asp Ser Cys Tyr Pro Asp 130 135

<210> 5 <211> 119 <212> Protein <213> Bull frog <220> <221> misc-feature <222> Synthetic polypeptide J chain <400> 5 Glu Gln Glu Tyr Ile Leu Ala Asn Asn Lys Cys Lys Cys Val Lys Ile Ser Ser Arg Phe Val Pro Ser Thr Glu Arg Pro Gly Glu Glu Ile Leu 25 Glu Arg Asn Ile Gln Ile Thr Ile Pro Thr Ser Ser Arg Met Xaa Ile 35 40 45 Ser Asp Pro Tyr Ser Pro Leu Arg Thr Gln Pro Val Tyr Asn Leu Trp Asp Ile Cys Gln Lys Cys Asp Pro Val Gln Leu Glu Ile Gly Gly Ile 70 75 Pro Val Leu Ala Ser Gln Pro Xaa Xaa Ser Xaa Pro Asp Asp Glu Cys 90 Tyr Thr Thr Glu Val Asn Phe Lys Lys Lys Val Pro Leu Thr Pro Asp 100 Ser Cys Tyr Glu Tyr Ser Glu 115 <210> 6 <211> 129 <212> Protein <213> Earthworm <220> <221> misc-feature <222> Synthetic polypeptide J chain <400> 6 Asn Lys Cys Met Cys Thr Arg Val Thr Ala Arg Ile Arg Gly Thr Arg 10 Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Tyr Ile Arg Ile Asn Val

Pro Leu Lys Asn Arg Gly Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg

Tyr Glu Asp Gly Val Val Thr Ala Thr Glu Thr Asn Ile Cys Tyr Pro 70 75 Asp Gln Gly Val Pro Gln Ser Cys Arg Asp Tyr Cys Pro Glu Leu Asp Arg Asn Lys Cys Tyr Thr Val Leu Val Pro Pro Gly Tyr Thr Gly Glu 105 Thr Lys Met Val Gln Asn Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp 120 . <210> 7 <211> 421 <212> DNA <213> Artificial Sequence <220> <221> CDS <222> (1)..(414) <220> <221> misc-feature <222> Description of Artificial Sequence: Synthetic polypeptide including target of "full length" TM cDNA <400> 7 GAT CAG GAA GAT GAA CGT ATT GTT CTG GTT GAC AAC AAG TGC AAG TGT 48 Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys 10 GCT CGT ATT ACT TCT AGA ATC ATC CGT AGC TCA GAG GAC CCA AAT GAA 96 Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu 20 GAT ATA GTC GAA CGT AAC ATC CGT ATC ATC GTC CCA CTG AAT AAC CGG 144 Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg 35 GAG AAT ATC TCA GAT CCT ACA AGT CCG TTG CGC ACA CGC TTC GTA TAC 192 Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr CAC CTG TCA GAT CTG TGT AAG AAG TGT GAT CCA ACA GAG GTA GAG CTG 240 His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu 65 70

Asn Gln Pro Val Tyr His Leu Ser Pro Ser Cys Lys Lys Cys Asp Pro

GA(C AAT Asr	CAC Glr	ATA 1 Ile	GTC Val	Thr	GCG Ala	ACT Thr	CAA	A AGO 1 Ser 90	Asn	ATI	TGC Cys	GAT Asp	GAG Glu 95	GAC Asp		288
AGC Ser	GCT Ala	ACA Thr	GAA Glu 100	Thr	TGC Cys	AGC Ser	ACC Thr	TAC Tyr 105	Asp	AGG Arg	AAC Asn	AAA Lys	TGC Cys 110	Tyr	ACG Thr		336
GCC Ala	GTG Val	GTT Val 115	Pro	CTC Leu	GTG Val	TAT Tyr	GGT Gly 120	GGA Gly	GAG Glu	ACA Thr	AAA Lys	ATG Met 125	GTG Val	GAA Glu	ACT Thr		384
		Thr				TGC Cys 135					ATTC						421
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<40 GAT Asp 1	CAG	3 AAG Lys	TGC Cys	AAG Lys 5	TGT Cys	GCT Ala	CGT Arg	ATT Ile	ACT Thr	TCT Ser	AGA Arg	ATC Ile	ATC Ile	CGT Arg 15	AGC Ser		48
TCA Ser	GAG Glu	GAC Asp	CCA Pro 20	AAT Asn	GAA Glu	GAT Asp	ATA Ile	GTC Val 25	GAA Glu	CGT Arg	AAC Asn	ATC Ile	CGT Arg 30	ATC Ile	ATC Ile		96
GTC Val	CCA Pro	CTG Leu 35	AAT Asn	AAC Asn	CGG Arg	GAG Glu	AAT Asn 40	ATC Ile	TCA Ser	GAT Asp	CCT Pro	ACA Thr 45	AGT Ser	CCG Pro	TTG Leu	:	144
CGC Arg	ACA Thr 50	CGC Arg	TTC Phe	GTA Val	TAC Tyr	CAC His 55	CTG Leu	TCA Ser	GAT Asp	CTG Leu	TGT Cys 60	AAG Lys	AAG Lys	GAT Asp	GAG Glu	:	192
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<400> 9 CTAGAATCAT CCGTAGCTCA GAGGACCCAA ATGAAGATAT AGTCGAACGT A	ACATCCGTA 60
TCATCGTCCC ACTGAATAAC CGGGAGAATA TCTCAGATCC TACAAGTCCG T	TGCGCACAC 120
GCTTCGTATA CCACCTGTCA	140
<210> 10 <211> 31 <212> DNA <213> Artificial Sequence	
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<400> 10 GATCAGAAGT GCAAGTGTGC TCGTATTACT T	31
<210> 11 <211> 44 <212> DNA <213> Artificial Sequence	
<220> <221> CDS <222> (1)(42)	
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TG	44

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CAAAAATGGT GGAAACTGCC CTTACGCCCG ATGCATGCTA CCCTGACTG
                                                                       109
<210> 13
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<213>
      Artificial Sequence
<220>
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<222>
      (1)..(282)
<220>
<221> misc-feature
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cDNA using L3
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                                                                       48
Asp Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser
 15
                     20
                                         25
TCA GAG GAC CCA AAT GAA GAT ATA GTC GAA CGT AAC ATC CGT ATC ATC
                                                                       96
Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile
                 35
GTC CCA CTG AAT AAC CGG GAG AAT ATC TCA GAT CCT ACA AGT CCG TTG
                                                                      144
Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu
             50
CGC ACA CGC TTC GTA TAC CAC CTG TCA GAT CTG TGT AAG AAG TGT GAT
                                                                      192
Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp
         65
CCA ACA GAG GTA GAG CTG GAC AAT CAG ATA GTC ACT GCG ACT CAA AGC
                                                                      240
Pro Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser
     80
                         85
                                             90
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AAC ATT TGC GAT GAG GAC AGC GCT ACA GAA ACC TGC TAC TGA	282
Asn Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr * 95 100 105	
ATTC	286
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(222) (1)(105)	
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95 100 105 110	
ATA GTC ACT GCG ACT CAA AGC AAC ATT TGC GAT GAG GAC AGC GCT ACA	96
Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser Ala Thr	
115 120 125	
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Leu Trp Thr	
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<221> misc-feature	
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GATCAGGAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGTGTGC TCGTATTACT	60
T	61

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<21	1>	61															
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	•				cque												
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		misc															
<22	2>	Desc	ript	ion	of A	rtif	icia	ıl Se	quen	ce:	Nucl	eoti	de s	eque	nce o	f Tr	S2
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<40	0 >	16															
GCG	ATGA	CGA	ССАТ	AAGG	כר כ	מממי	GGAG	ים ככ	ייייכיייא	СТСТ	тсс	CCCT	ССТ	~~~	GGCAA	אל	~ 0
			00				OGAC	in cc	IGIA	CIGI	100	.GCC1	CGI	GAAC	AAJDD.	A	60
y Cun	~~~	מחנים ע	aaaa	a	m 2 2	a , a a	- CTI-CTI			~							
ACI	GCGG	AII	CCCG	GAAG	TA A	CACC	CTCI	C AG	TGCG	CTAA	. TAA	AGGC	TGC	TGTT	TTGAT	3	120
				_													
ACA	CGGT	ACG	GGGC	GTTC	CG T	GGTG	CTTC	T AC	CCCA	ATAC	AAT	TGAC	GTT	CCGC	CTGAA	3 .	180
AAG	AGTG	CGA	GCCG	TAAG													198
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		Prot															
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100	~+ h //	mw.	TIPL	TOIL	OL A	TULL	ICIa	ı se	quen	ce:	Synt	neti	с ро	туре	ptide	Οİ	"tull
TEIL	g cm.	TM	CDNA														
	_																
<40		17									`						
Asp	Gln	Glu	Asp	Glu	Arg	Ile	Val	Leu	Val	Asp	Asn	Lys	Cys	Lys	Cys		
1				5					10				_	15	-		
																·	
Ala	Ara	Tle	Thr	Ser	Ara	Tle	Tle	Δrα	Ser	Ser	Gl ₁₁	Λαn	Dro	Asn	01		
	5		20		5			25	UCI	DCI	Olu	Asp		ASII	GIU		
			20					25					30				
	~ 1			_	_			_	_								
Asp	ше		GIU	Arg	Asn	Ile								Asn	Arg		
		35					40					45					
Glu	Asn	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu	Ara	Thr	Ara	Phe	Val	Tyr		
	50			_		55					60	5			-1-		
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77.5	пси	561	Asp	ьец		гуѕ	ьуѕ	Cys	Asp		Thr	GIu	Val	Glu	Leu		
65					70					75					80		
Asp	Asn	Gln	Ile	Val	Thr	Ala	Thr	Gln	Ser	Asn	Ile	Cys	Asp	Glu	Asp		
				85					90			•		95	r		
														,,			
Ser	Ala	Thr	Glu	Thr	Cve	Ser	Thr	ጥኒታው	Δας	Δ~~	7~~	T •••	C+	Tyr	mb		
				T 11T	Cys	DCT	TIIT		мsр	Arg	ASII	гуя		ıyr	inr		
			100					105					110				
			_	_													
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Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile
             20
                                 25
Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu
         35
                             40
Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Asp Glu
Asp Ser Ala Thr Glu Thr Cys
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135

130

Leu

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fragment
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<210> 22
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fragment
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    Cys Tyr Pro Asp
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cDNA using L3
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Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile
             20
                                25
Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu
                             40
Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp
Pro Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser
65
                    70
                                        75
Asn Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr
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<210> 24
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<221> misc-feature

<222> Description of Artificial Sequence: Synthetic polypeptide of L3 fragment

<400> 24

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Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser Ala Thr 25

Leu Trp Thr

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fragment
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                 20
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     Cys Ser Asp Asp Asp Lys Ala Gln Thr Glu Thr Cys Thr Val Ala
                                        10
                                                            15
     Pro Arg Glu Arg Gln Asn Cys Gly Phe Pro Gly Val Thr Pro Ser Gln
     Cys Ala Asn Lys Gly Cys Cys Phe Asp Asp Thr Val Arg Gly Val Pro
     Trp Cys Phe Tyr Pro Asn Thr Ile Asp Val Pro Pro Glu Glu Glu Cys
         50
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of "full length" TM cDNA
<400> 27
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60

CTAGTCCTTC TACTTGCATA ACAAGACCAA CTGTTGTTCA CGTTCACACG AGCATAATGA

AGATCTTAGT AGGCATCGAG TCTCCTGGGT TTACTTCTAT ATCAGCTTGC ATTGTAGGC	CA 120
TAGTAGCAGG GTGACTTATT GGCCCTCTTA TAGAGTCTAG GATGTTCAGG CAACGCGTG	ST _. 180
GCGAAGCATA TGGTGGACAG TCTAGACACA TTCTTCACAC TAGGTTGTCT CCATCTCGA	AC 240
CTGTTAGTCT ATCAGTGACG CTGAGTTTCG TTGTAAACGC TACTCCTGTC GCGATGTCT	TT 300
TGGACGTCGT GGATGCTATC CTTGTTTACG ATGTGCCGGC ACCAAGGCGA GCACATACC	A 360
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TTACTTCTAT ATCAGCTTGC ATTGTAGGCA TAGTAGCAGG GTGACTTATT GGCCCTCTT	A 120
TAGAGTCTAG GATGTTCAGG CAACGCGTGT GCGAAGCATA TGGTGGACAG TCTAGACACA	A 180
TTCTTCCTAC TCCTGTCGCG ATGTCTTTGG ACGACTTAA	219
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of D 1.1 fragment
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TCTTCACGTT CACACGAGCA TAATGAAGAT C
                                                                      31
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<211> 44
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<220>
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<222> Complementary nucleotide sequence of L3D fragment
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ACACATTCTT CCTACTTCTC AGGCGATGTC TTTGGACGAC TTAA
                                                                      44
<210> 32
<211> 117
<212> DNA
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of T4 fragment
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ACGTCGTGGA TGCTATCCTT GTTTACGATG TGCCGGCACC AAGGCGAGCA CATACCACCT
                                                                      60
CTCTGTTTTT ACCACCTTTG ACGGGAATGC GGGCTACGTA CGATGGGACT GACTTAA
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TTACTTCTAT ATCAGCTTGC ATTGTAGGCA TAGTAGCAGG GTGACTTATT GGCCCTCTTA	120
TAGAGTCTAG GATGTTCAGG CAACGCGTGT GCGAAGCATA TGGTGGACAG TCTAGACACA	180
TTCTTCACAC TAGGTTGTCT CCATCTCGAC CTGTTAGTCT ATCAGTGACG CTGAGTTTCG	240
TTGTAAACGC TACTCCTGTC GCGATGTCTT TGGACGATGA CT	282
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ACTCAAAGCA ACATTTGCGA TGAGGACAGC GCTACACTTT GGACG	60 105
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AGATC	65

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of TpS2
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                                                                      60
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                                                                      120
CTACTGTGCC ATGCCCCGCA AGGCACCACG AAGATGGGGT TATGTTAACT GCAAGGCGGA
                                                                      180
CTTCTTCTCA CGCTCGGCAT TCTTAA
                                                                     206
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substantial \beta-sheet character
<400> 37
    Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys
<210> 38
<211> 7
<212> Protein
<213> Tobacco etch virus
<220>
<221> misc-feature
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<400> 38
    Glu Asn Leu Tyr Phe Gln Ser
                    5
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<210> 39
<211> 11
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from pro-cathepsin E
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    Lys Ala His Lys Val Asp Met Val Gln Tyr Thr
                    5
<210> 40
<211> 4
<212> Protein
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<400> 40
    Val Gln Tyr Thr
    1
<210> 41
<211> 6
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<213> Human
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<222> Linker from polyimmunoglobulin receptor
<400> 41
    Glu Lys Ala Val Ala Asp
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<210> 42
<211> 131
<212> DNa
<213> Artificial Sequence
<220> CDS
<221> 1..78
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signal from pMelBac
<400> 42
ATG AAA TTC TTA GTC AAC GTT GCC CTT TTT ATG GTC GTA TAC ATT TCT
                                                                       48
Met Lys Phe Leu Val Asn Val Ala Leu Phe Met Val Val Tyr Ile Ser
                 40
                                     45
TAC ATC TAT GCG GAT CCG AGC TCG AGT GCT CTAGATCTGC AGCTGGTACC
                                                                       98
Tyr Ile Tyr Ala Asp Pro Ser Ser Ser Ala
             55
ATGGAATTCG AAGCTTGGAG TCGACTCTGC TGA
                                                                      131
<210> 43
<211> 26
<212> Protein
<213> Artificial Sequence
<220>
<221> misc-feature
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secretion signal from pMelBac
<400> 43
Met Lys Phe Leu Val Asn Val Ala Leu Phe Met Val Val Tyr Ile Ser
                                     10
                                                         15
Tyr Ile Tyr Ala Asp Pro Ser Ser Ser Ala
             20
<210> 44
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<222> Description of Artificial Sequence: Endomembrane retention signal
<400> 44
    Lys Asp Glu Leu
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<210> 45
<211> 16
<212> Protein
<213> Human
<220>
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<222> Residues 585-600 of polyimmunoglobulin receptor
<400> 45
     Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu Lys Ala Val Ala Asp
                                             10
<210> 46
<211> 61
<212> DNA
<213> Artificial Sequence
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GATCAGGAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGTGTGC TCGTATTACT
                                                                      60
Т
                                                                      61
<210> 47
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CTAGAAGTAA TACGAGCACA CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC
                                                                      60
Т
                                                                      61
<210> 48
<211> 31
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<221> misc-feature
<222> Description of Artificial Sequence: Oligonucleotide 1.1
<400> 48
GATCAGAAGT GCAAGTGTGC TCGTATTACT T
                                                                      31
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<213>	Artificial Sequence	
	•	
<220>		
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	Description of Artificial Sequence: Oligonucleotide 1.2	
10007	beboriperon of Arctificial Bequence. Offgonucleotide 1.2	
<400>	49	
CIAGAA	GTAA TACGAGCACA CTTGCACTTC T	31
	50	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
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<222>		
,,	200011P010M 01 MICHIELLA BEQUENCE. OHIGONACIEOCIAE 1.28EL	
<400>	50	
	GAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGTCCGC TCGTATTACT	
GAICAGG	BAAG AIGAACGIAI IGIICIGGII GACAACAAGI GCAAGICCGC TCGTATTACT	60
Т		
1		61
<210>		
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	2	
<400>	51	
	TAA TACGAGCGGA CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC	60
	Indiados. Circaciro rigidancea Gancaniaco ricarcirco	00
Т		<i>-</i> -
-		61

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<210> 52
 <211> 61
 <212> DNA
 <213> Artificial Sequence
<220>
<221> misc-feature
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<400> 52
GATCAGGAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGGTTGC TCGTATTACT
                                                                       60
Т
                                                                       61
<210> 53
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CTAGAAGTAA TACGAGCAAC CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC
                                                                       60
Т
                                                                       61
<210> 54
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CTAGAATCAT CCGTAGCTCA GAGGACCCAA ATGAAGATAT AGTCGAA
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GATACGGATG TTACGTTCGA CTATATCTTC ATTTGGGTCC TCTGAGCTAC GGATGATT
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 <212> DNA
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 <221> misc-feature
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 <400> 56
 CGTAACATCC GTATCATCGT CCCACTGAAT AACCGGGAGA ATATCTCAG
                                                                       49
 <210> 57
 <211> 49
 <212> DNA
< <213> Artificial Sequence
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 <400> 57
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                                                                       49
 <210> 58
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 ACGGACTTGT AGGATCTGAG ATATTCTCCC GGTTATTCAG TGGGACGAT
                                                                       49
 <210> 59
 <211> 49
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ACGGACTTGT AGGATCTGAG ATGTGCTCCC GGTTATTCAG TGGGACGAT
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<211> 44
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                                                                       44
<210> 61
<211> 33
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GATCTGACAG GTGGTATACG AAGCGTGTGC GCA
                                                                       33
<210> 62
<211> 60
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<400> 62
GATCTGTGTA AGAAGTGTGA TCCAACAGAG GTAGAGCTGG ACAATCAGAT AGTCACTGCA
                                                                       60
<210> 63
<211> 44
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<222> Description of Artificial Sequence: Oligonucleotide 9L3\Delta
<400> 63
GATCTGTGTA AGAAGGATGA GGACAGCGCT ACAGAAACCT GCTG
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<213>	Artificial Sequence	
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<220>		
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<222>	Description of Artificial Sequence: Oligonucleotide 10L3 Δ	
	or and the second of the secon	
<400>	64	
AATTC	AGCAG GTTTCTGTAG CGCTGTCCTC ATCCTTCTTA CACA	
	THE CACA	44
<210>	65	
<211>	62	
<212>		
	Artificial Sequence	
1207	in our rough bequence	
<220>		
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	Description of Artificial Sequence: Oligonucleotide 9L3AKDEL	
12227	bescription of Artificial Sequence: Oligonucleotide 9L3AKDEL	
<400>	65	
	TGTA AGAAGGATGA GGACAGCGCT ACAGAAACCT GCTACGAGAA GGATGAGCTG	
0111010	TOTA ADARGGATGA GGACAGCGCT ACAGAAACCT GCTACGAGAA GGATGAGCTG	60
TG		
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\Z13/	Artificial Sequence	
<220>		
	misc-feature	
<222>		
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<400>	66	
inii i Ch	CAGC TCATCCTTCG CGTCGCAGGT TTCTGTAGCG CTGTCCTCAT CCTTCTTACA	60
CA		
Ch		62
<210>	67	
<211>	59	
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<222>		
/	Description of Artificial Sequence: Oligonucleotide $9.2\Delta3$	
<400>	67	
	GTA AGAAGTCTGA TATCGATGAA GATTCCGCTA CAGAAACCTG CAGCACATG	
		59

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AATTCATGTG CTGCAGGTTT CTGTAGCGGA ATCTTCATCG ATATCAGACT TCTTACACA
                                                                      59
<210> 69
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<400> 69
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CTAA
                                                                        64
<210> 70
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<400> 70
AATCTTCATC GATATCAGAC TTCTTAGACA
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<210> 71
 <211> 64
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                                                                       60
CTAA
                                                                       64
<210> 72
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<210> 73
<211> 41
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ATTGTCCAGC TCTACCTCTG TTGGATCACA CTTCTTACAC A
                                                                       41
<210> 74
<211> 46
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<400> 74
ACTCAAAGCA ACATTTGCGA TGAGGACAGC GCTACAGAAA CCTGCA
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<210> 75
 <211> 57
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<400> 75
GGTTTCTGTA GCGCTCTGCT CATCGCAAAT GTTGCTTTGA GTCGCAGTGA CTATCTG
                                                                      57
<210> 76
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<400> 76
GCACCTACGA TAGGAACAAA TGCTACACGG CCGTGGTTCC GCTCGTGTAT GGTGGAGAG
                                                                59
<210> 77
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GAGCGGAACC ACGGCCGTGT AGCATTTGTT CCTATCGTAG GTGCTGCA
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<210> 78
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ACAAAAATGG TGGAAACTGC CCTTACGCCC GATGCATGCT ATCCGGACTG
                                                                     50
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\Z1U >	19	
<211>	69	
<212>	DNA	
<213>	Artificial Sequence	
12.207	interretar bequence	
<220>		
	milian for a	
<221>		
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<400>	79	
AATTCA	AGTCC GGATAGCATG CATCGGGCGT AAGGGCAGTT TCCACCATTT TTGTCTCTCC	60
		•
ACCATA	CAC	69
		09
<210>	80	
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<212>		
	DNA	
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	1 January Johnson Officender Coulde 13/0000	
<400>	80	
	ATGG TGGAAACTGC CCTTACGCCC GATGCATGCT ATCCGGACAA GGATGAATTG	
	ATOU TOURANCIUC CCITACUCCC GAIGCAIGCT ATCCGGACAA GGATGAATTG	60
TG		
10		62
	81	
<211>	81	
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<213>	Artificial Sequence	
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	misc-feature	
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\424 /	Description of Artificial Sequence: Oligonucleotide 16KDEL	
.400	21	
<400>	81	
AATTCA	CAAT TCATCCTTGT CCGGATAGCA TGCATCGGGC GTAAGGGCAG TTTCCACCAT	60
TTTTGT	CTCT CCACCATACA C	0.1

<210>	82	
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<220>		
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	· J	
<400>	82	
GATCAG	GTCG CTGCCATCCA AGACCCGAGG CTGTTCGCCG AAGAGAAGGC CGTCGCTGAC	60
TCCAAG'	IGCA AGTGTGCTCG TATTACTT	88
<210>	83	
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	misc-feature	
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CTAGAAC	TAA TACGAGCACA CTTGCACTTG GAGTCAGCGA CGGCCTTCTC TTCGGCGAAC	60
AGCCTCC	GGGT CTTGGATGGC AGCGACCT	88
<210>	84	
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	Protein	
	Artificial Sequence	
12107	rectificate bequence	
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	misc-feature	
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	r bequence inducted targeting sequence I	
<400>	84	
Су	s Ala Ala Pro Lys Lys Arg Lys Val	
1	5 10	

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<210> 85
<211> 22
<212> Protein
<213> Artificial Sequence
<220>
<221> misc-feature
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     Cys Ala Ala Lys Arg Pro Pro Ala Ala Ile Lys Lys Ala Ala Ala Gly
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     Gln Ala Lys Lys Lys
                 20
<210> 86
<211> 4
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<222> Description of Artificial Sequence: HDEL linker sequence for
intracellular targeting
<400> 86
    His Asp Glu Leu
<210> 87
<211> 77
<212> DNA
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GCGATGACGA CGATAAGGCC CAAACGGAGA CCTGTACTGT TGCGCCTCGT GAACGGCAAA
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ACTGCGGATT CCCGGAA
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<212>	DNA	
	Artificial Sequence	
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	misc-feature	
\222 <i>></i>	Description of Artificial Sequence: Oligonucleotide Tp2	
.400-		
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GTTTTG	CCGT TCACGAGGCG CAACAGTACA GGTCTCCGTT TGGGCCTTAT CGTCGTCATC	60
GCTTCA		66
<210>	89	
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<220>		
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	Description of Artificial Sequence: Oligonucleotide Tp3	
	e de la contraction de la cont	
<400>	89	
	CCCT CTCAGTGCGC TAATAAAGGC TGCTGTTTTG ATGACACGGT ACGGGGCGTT	
	GOOT GICAGIOGGG TAATAAAGGC IGCIGIIIIG ATGACACGGT ACGGGGCGTT	60
СССТСС	TGCT TC	
000100		72
	•	
<210>	90	
<211>		
<211>		
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000		
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CGGGAAT	TCCG CA	72

(210)	91.	
<211>	49	
<212>		
(213)	Artificial Sequence	
<220>		
<221>	misc-feature	
<222>	Description of Artificial Sequence: Oligonucleotide Tp5	
	i and adjusted of the state of	
<400>	91	
	- <del>-</del>	
IACCC	CAATA CAATTGACGT TCCGCCTGAA GAAGAGTGCG AGCCGTAAG	49
<210>		
<211>	68	
<212>	DNA	
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	•	
<220>		
	misc-feature	
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		•
<400>		
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		00
CACGGA	AC	<b>~</b> 0
		68
<210>	93	
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	Protein	
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<220>		
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	i bequence: Synchetic peptide linker	
<400>	93	
1	al Ala Val Gln Ser Ala Gly Thr Pro Ala Ser Gly Ser	
1	5 10	-